
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=12; day=17; hr=14; min=3; sec=38; ms=706;]

Validated By CRFValidator v 1.0.3

Application No: 10568055 Version No: 2.0

Input Set:

Output Set:

Started: 2009-11-30 17:47:00.563

Finished: 2009-11-30 17:47:03.924

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 361 ms

Total Warnings: 47

Total Errors: 0

No. of SeqIDs Defined: 92

Actual SeqID Count: 92

Error code		Error Description									
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(1)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(2)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(3)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(4)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(5)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(6)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(7)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(8)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(9)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(10)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(11)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(12)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(13)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(14)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(15)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(16)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(17)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(18)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(19)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(20)

Input Set:

Output Set:

Started: 2009-11-30 17:47:00.563 **Finished:** 2009-11-30 17:47:03.924

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 361 ms

Total Warnings: 47
Total Errors: 0
No. of SeqIDs Defined: 92

Actual SeqID Count: 92

Error code		Error Description									
		This error has occured more than 20 times, will not be displayed									
W	402	Undefined organism found in <213> in SEQ ID (33)									
W	402	Undefined organism found in <213> in SEQ ID (34)									
W	402	Undefined organism found in <213> in SEQ ID (35)									
W	402	Undefined organism found in <213> in SEQ ID (36)									
W	402	Undefined organism found in <213> in SEQ ID (37)									
W	402	Undefined organism found in <213> in SEQ ID (38)									
W	402	Undefined organism found in <213> in SEQ ID (66)									
W	402	Undefined organism found in <213> in SEQ ID (67)									
W	402	Undefined organism found in <213> in SEQ ID (68)									
W	402	Undefined organism found in <213> in SEQ ID (69)									
W	402	Undefined organism found in <213> in SEQ ID (70)									
W	402	Undefined organism found in <213> in SEQ ID (71)									

SEQUENCE LISTING

```
<110> Cambridge University Technical Services Limited
      Doherty, Aidan
      Della, Marina
      Weller, Geoffrey
      Jackson, Stephen
<120> Prokaryotic DNA Repair Ligases
<130> 6947-73362-01
<140> 10568055
<141> 2006-09-27
<150> PCT/GB2004/003349
<151> 2004-08-02
<150> US 60/494,088
<151> 2003-08-12
<160> 92
<170> PatentIn version 3.1
<210> 1
<211> 10
<212> PRT
<213> Artificial sequence
<220>
<223> Conserved motif
<400> 1
Arg Leu Val Phe Asp Leu Asp Pro Gly Glu
<210> 2
<211> 10
<212> PRT
<213> Artificial sequence
<220>
<223> Conserved motif
Ser Gly Ser Lys Gly Leu His Leu Tyr Thr
               5
                                   10
<210> 3
<211> 6
<212> PRT
<213> Artificial sequence
<220>
<223> Conserved motif
<400> 3
```

Lys Val Phe Val Asp Trp

```
<210> 4
<211> 20
<212> DNA
<213> Artificial sequence
<220>
<223> Primer
<400> 4
                                                                    20
atgcgagcca tttggacggg
<210> 5
<211> 25
<212> DNA
<213> Artificial sequence
<220>
<223> Primer
<400> 5
                                                                    25
ggatcctcac ggaggcgttg ggacg
<210> 6
<211> 20
<212> DNA
<213> Artificial sequence
<220>
<223> Primer
<400> 6
                                                                    20
atgggttcgg cgtcggagca
<210> 7
<211> 26
<212> DNA
<213> Artificial sequence
<220>
<223> Primer
<400> 7
tcctcattcg cgcaccacct cactgg
                                                                    26
<210> 8
<211> 15
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 8
ctgcagctga tgcgc
                                                                    15
<210> 9
<211> 20
<212> DNA
```

5

<213> Artificial sequence

1

```
<220>
<223> Oligonucleotide
<400> 9
atccggcgca tcagctgcag
                                                                     20
<210> 10
<211> 25
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 10
                                                                     25
agtcgatcct gcgcatcatc tgcag
<210> 11
<211> 41
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 11
                                                                     41
acceggggat cegtacagte tateeggege ateagetgea g
<210> 12
<211> 50
<212> DNA
<213> Artificial sequence
<220>
<223> 50mer substrate
<400> 12
                                                                     50
gtaacaaagt ttggattgct actgaccgct ctcgtgctcg tcgctgcgtt
<210> 13
<211> 50
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 13
                                                                     50
gtctgtctca ctattagaac cctttagagt catgcgtcgc gaggcaacgc
<210> 14
<211> 43
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 14
                                                                     43
gcctcgcgac gcatgactct aaagggttct aatagtgaga cag
<210> 15
<211> 41
```

```
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 15
gcgacgagca cgagagcggt cagtagcaat ccaaactttg t
                                                                     41
<210> 16
<211> 50
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 16
gtaacaaagt ttggattgct actgaccgct ctcgtgctcg tcgctgcgtt
                                                                     50
<210> 17
<211> 52
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 17
                                                                     52
ctgtctgtct cactattaga accctttaga gtcatgcgtc gcgaggcaac gc
<210> 18
<211> 20
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 18
                                                                     20
gaaaccacgt accggcgtgt
<210> 19
<211> 13
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 19
                                                                     13
ctttggtcga tgg
<210> 20
<211> 26
<212> DNA
<213> Artificial sequence
<220>
<223> Oligonucleotide
<400> 20
```

ctgcag	atca tgcgccggat tgcccc	26					
<210>	21						
<211>	17						
<212>	DNA						
<213>	Artificial sequence						
1000							
<220>							
<223>	Oligonucleotide						
<400>	21	17					
gaegrei	tagt acgcggc	17					
<210>	22						
<211>	20						
	DNA						
	Artificial sequence						
-210	THE LEGICAL BONNESS						
<220>							
<223>	Primer						
<400>	22						
caagtai	tgga tctcgaggtt	20					
<210>	23						
<211>	20						
<212>	DNA						
<213>	Artificial sequence						
<220>							
<223>	Primer						
<400>	23						
ctgttc	taga ggtacctagt	20					
<210>	24						
<211>	20						
<212>	DNA						
<213>	Artificial sequence						
*000							
<220>	Podence						
	Primer						
<400>		2.0					
ccttaa	gttg aacggagtcc	20					
<210>	25						
<211>							
<212>							
	Artificial sequence						
-220							
<220>							
	Primer						
<400>							
	cttgactage gcactaceag 20						
-							
<210>	26						
<211>	21						
<212>	DNA						
<213>	Artificial sequence						

```
<223> Primer
<400> 26
ggcaggagaa ttttcagcat c
                                                                  21
<210> 27
<211> 8
<212> PRT
<213> Bacillus subtilis
<400> 27
Glu Val Lys Tyr Asp Gly Tyr Arg
     5
<210> 28
<211> 8
<212> PRT
<213> Bacillus subtilis
<400> 28
Leu Thr Leu Asp Gly Glu Ile Val
            5
<210> 29
<211> 12
<212> PRT
<213> Bacillus subtilis
<400> 29
Cys Phe Leu Ala Phe Asp Leu Leu Glu Arg Ser Gly
              5
                                 10
<210> 30
<211> 5
<212> PRT
<213> Bacillus subtilis
<400> 30
Glu Gly Ile Val Ala
<210> 31
<211> 11
<212> PRT
<213> Bacillus subtilis
<400> 31
Trp Leu Lys Tyr Lys Asn Phe Lys Gln Ala Tyr
             5
                                10
<210> 32
<211> 11
<212> PRT
<213> Bacillus subtilis
<400> 32
Ile Gly Phe Glu Phe Gln Met Asp Trp Thr Glu
```

<220>

```
5
                                 10
<210> 33
<211> 8
<212> PRT
<213> Bacillus halodurans
<400> 33
Glu Val Lys Tyr Asp Gly Phe Arg
<210> 34
<211> 8
<212> PRT
<213> Bacillus halodurans
<400> 34
Ile Thr Ile Asp Gly Glu Leu Val
<210> 35
<211> 12
<212> PRT
<213> Bacillus halodurans
<400> 35
Thr Leu Leu Ala Phe Asp Ile Leu Glu Leu Lys Gly
     5
                                10
<210> 36
<211> 5
<212> PRT
<213> Bacillus halodurans
<400> 36
Glu Gly Val Val Ala
<210> 37
<211> 11
<212> PRT
<213> Bacillus halodurans
<400> 37
Trp Leu Lys Lys Lys Asn Phe Arg Gln Val Thr
    5
<210> 38
<211> 11
<212> PRT
<213> Bacillus halodurans
<400> 38
His Arg Phe Arg Leu Asp Val Lys Pro Ala Gln
```

```
<212> PRT
<213> Mycobacterium tuberculosis
<400> 39
Glu Pro Lys Trp Asp Gly Phe Arg
<210> 40
<211> 8
<212> PRT
<213> Mycobacterium tuberculosis
<400> 40
Cys Val Ile Asp Gly Glu Ile Ile
              5
<210> 41
<211> 12
<212> PRT
<213> Mycobacterium tuberculosis
<400> 41
Ser Phe Ile Ala Phe Asp Leu Leu Ala Leu Gly Asp
<210> 42
<211> 5
<212> PRT
<213> Mycobacterium tuberculosis
<400> 42
Asp Gly Val Ile Ala
<210> 43
<211> 11
<212> PRT
<213> Mycobacterium tuberculosis
<400> 43
Met Phe Lys Ile Lys His Leu Arg Thr Ala Asp
           5
<210> 44
<211> 11
<212> PRT
<213> Mycobacterium tuberculosis
<400> 44
Thr Ala Gln Phe Asn Arg Trp Arg Pro Asp Arg
<210> 45
<211> 8
<212> PRT
<213> Bacillus subtilis
```

<211> 8

```
Glu Leu Lys Phe Asp Gly Ile Arg
<210> 46
<211> 8
<212> PRT
<213> Bacillus subtilis
<400> 46
Thr Val Leu Asp Gly Glu Val Ile
     5
<210> 47
<211> 12
<212> PRT
<213> Bacillus subtilis
<400> 47
Val Tyr Cys Val Phe Asp Val Ile Tyr Lys Asp Gly
<210> 48
<211> 5
<212> PRT
<213> Bacillus subtilis
<400> 48
Glu Gly Ile Val Ile
<210> 49
<211> 11
<212> PRT
<213> Bacillus subtilis
<400> 49
Trp Leu Lys Val Ile Asn Tyr Asp Tyr Thr Glu
<210> 50
<211> 8
<212> PRT
<213> Pseudomonas aeruginosa
<400> 50
Glu Leu Lys Leu Asp Gly Tyr Arg
<210> 51
<211> 8
<212> PRT
<213> Pseudomonas aeruginosa
<400> 51
Ser Trp Leu Asp Gly Glu Leu Val
```

<400> 45

```
5
1
<210> 52
<211> 12
<212> PRT
<213> Pseudomonas aeruginosa
<400> 52
Leu Tyr Val Leu Phe Asp Leu Pro Tyr His Glu Gly
<210> 53
<211> 5
<212> PRT
<213> Pseudomonas aeruginosa
<400> 53
Glu Gly Val Ile Gly
<210> 54
<211> 11
<212> PRT
<213> Pseudomonas aeruginosa
<400> 54
Trp Ile Lys Leu Lys Cys Gln Leu Arg Gln Glu
          5
                                 10
<210> 55
<211> 11
<212> PRT
<213> Pseudomonas aeruginosa
<400> 55
Ala Arg Glu Val Thr Gly Glu Arg Pro Ala Gly
                                  10
<210> 56
<211> 8
<212> PRT
<213> Mycobacterium tuberculosis
<400> 56
Glu Gly Lys Trp Asp Gly Tyr Arg
<210> 57
<211> 8
<212> PRT
<213> Mycobacterium tuberculosis
<400> 57
Val Val Leu Asp Gly Glu Ala Val
```

```
<212> PRT
<213> Mycobacterium tuberculosis
<400> 58
Glu Phe Trp Ala Phe Asp Leu Leu Tyr Leu Asp Gly
<210> 59
<211> 5
<212> PRT
<213> Mycobacterium tuberculosis
<400> 59
Glu Gly Val Ile Ala
<210> 60
<211> 11
<212> PRT
<213> Mycobacterium tuberculosis
<400> 60
Trp Val Lys Asp Lys His Trp Asn Thr Gln Glu
<210> 61
<211> 10
<212> PRT
<213> Mycobacterium tuberculosis
<400> 61
Ser Ser Trp Arg Gly Leu Arg Pro Asp Lys
              5
<210> 62
<211> 6
<212> PRT
<213> Artificial sequence
<220>
<223> Bact ATP Consensus
<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is hydrophobic
<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is hydrophobic
<400> 62
Lys Xaa Asp Gly Xaa Arg
```

<211> 12

```
<211> 6
<212> PRT
<213> Artificial sequence
<220>
<223> Bact ATP Consensus
<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is hydrophobic
<220>
<221> MISC_FEATURE
<222> (5)..(6)
<223> Xaa is hydrophobic
<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is polar
<400> 63
Xaa Xaa Gly Glu Xaa Xaa
<210> 64
<211> 4
<212> PRT
<213> Artificial sequence
<220>
<223> Bact ATP Consensus
<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is hydrophobic
<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is hydrophobic
<400> 64
Xaa Phe Asp Xaa
<210> 65
<211> 5
<212> PRT
<213> Artificial sequence
<220>
<223> Bact ATP Consensus
<220>
<221> MISC_FEATURE
<222> (3)..(5)
```

```
<223> Xaa is hydrophobic
<400> 65
Glu Gly Xaa Xaa Xaa
<210> 66
<211> 8
<212> PRT
<213> T7
<400> 66
Glu Ile Lys Tyr Asp Gly Val Arg
<210> 67
<211> 8
<212> PRT
<213> T7
<400> 67
Phe Met Leu Asp Gly Glu Leu Met
<210> 68
<211> 10
<212> PRT
<213> T7
<400> 68
His Ile Lys Leu Tyr Ala Ile Leu Pro Leu
    5
<210> 69
<211> 5
<212> PRT
<213> T7
<400> 69
Glu Gly Leu Ile Val
        5
<210> 70
<211> 11
<212> PRT
<213> T7
<400> 70
Trp Trp Lys Met Lys Pro Glu Asn Glu Ala Asp
1 5
<210> 71
<211> 10
<212> PRT
<213> T7
```

```
<400> 71
Pro Ser Phe Val Met Phe Arg Gly Thr Glu
<210> 72
<211> 10
<212> PRT
<213> Mycobacterium tuberculosis
<400> 72
Arg Leu Val Phe Asp Leu Asp Pro Gly Glu
     5
<210> 73
<211> 10
<212> PRT
<213> Mycobacterium tuberculosis
<400> 73
Ser Gly Ser Lys Gly Leu His Leu Tyr Thr
             5
<210> 74
<211> 6
<212> PRT
<213> Mycobacterium tuberculosis
<400> 74
Lys Val Phe Val Asp Trp
<210> 75
<211> 10
<212> PRT
<213> Homo sapiens
<400> 75
Glu Leu Val Phe Asp Ile Asp Met Thr Asp
             5
                                10
<210> 76
<211> 10
<212> PRT
<213> Homo sapiens
<400> 76
Ser Gly Arg Arg Gly Val His Cys Trp Val
     5
<210> 77
<211> 6
<212> PRT
<213> Homo sapiens
<400> 77
Phe Pro Arg Leu Asp Ile
               5
```

```
<211> 6
<212> PRT
<213> Mus musculus
<400> 78
Phe Pro Arg Leu Asp Val
<210> 79
<211> 10
<212> PRT
<213> Drosophila melanogaster
<400> 79
Ser Gly Arg Arg Gly Ile His Cys Trp Val
      5
                          10
<210> 80
<211> 6
<212> PRT
<213> Drosophila melanogaster
<400> 80
Tyr Pro Arg Leu Asp Ile
<210> 81
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae
<400> 81
Glu Leu Val Phe Asp Ile Asp Met Asp Asp
<210> 82
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae
<400> 82
Ser Gly Arg Arg Gly Ala His Cys Trp Val
<210> 83
<211> 6
<212> PRT
<213> Saccharomyces cerevisiae
<400> 83
Tyr Pro Lys Leu Asp Val
<210> 84
<211> 10
```

<210> 78

```
<212> PRT
<213> Schizosaccharomyces pombe
Ser Gly Arg Arg Gly Ile His Ala Trp Ile
               5
<210> 85
<211> 6
<212> PRT
<213> Schizosaccharomyces pombe
<400> 85
Tyr Pro Arg Leu Asp Val
<210> 86
<211> 13
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligomer
<400> 86
ggtacgtggt ttc
                                                                     13
<210> 87
<211> 17
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 87
cggcgcatga tctgcag
                                                                     17
<210> 88
<211> 20
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 88
                                                                     20
gaaaccacgt accggggtgt
<210> 89
<211> 39
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligomer
<400> 89
                                                                     39
ctgcagatca tgcgccggat tgccccggta cgtggtttc
```

```
<211> 39
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 90
gaaaccacgt accggggcaa tccggcgcat gatctgcag
<210> 91
<211> 759
<212> PRT
<213> Mycobacterium tuberculosis
<400> 91
Met Gly Ser Ala Ser Glu Gln Arg Val Thr Leu Thr Asn Ala Asp Lys
                     10
Val Leu Tyr Pro Ala Thr Gly Thr Thr Lys Ser Asp Ile Phe Asp Tyr
            25
Tyr Ala Gly Val Ala Glu Val Met Leu Gly His Ile Ala Gly Arg Pro
                     40
      35
Ala Thr Arg Lys Arg Trp Pro Asn Gly Val Asp Gln Pro Ala Phe Phe
   50 55 60
Glu Lys Gln Leu Ala Leu Ser Ala Pro Pro Trp Leu Ser Arg Ala Thr
      70
                    75
Val Ala His Arg Ser Gly Thr Thr Tyr Pro Ile Ile Asp Ser Ala
            85
                       90
Thr Gly Leu Ala Trp Ile Ala Gln Gln Ala Ala Leu Glu Val His Val
                105 110
         100
Pro Gln Trp Arg Phe Val Ala Glu Pro Gly Ser Gly Glu Leu Asn Pro
                     120
      115
                                     125
Gly Pro Ala Thr Arg Leu Val Phe Asp Leu Asp Pro Gly Glu Gly Val
   130 135 140
Met Met Ala Gln Leu Ala Glu Val Ala Arg Ala Val Arg Asp Leu Leu
```

155

160

145

150

39

Ala Asp Ile Gly Leu Val Inr Phe Pro Val Info Inr Ser Gly Ser Lys Gly Leu His Leu His Leu Tyr Thr 180 Pro 180 P

Trp Ala Glu Leu Asp Asp Pro Ala